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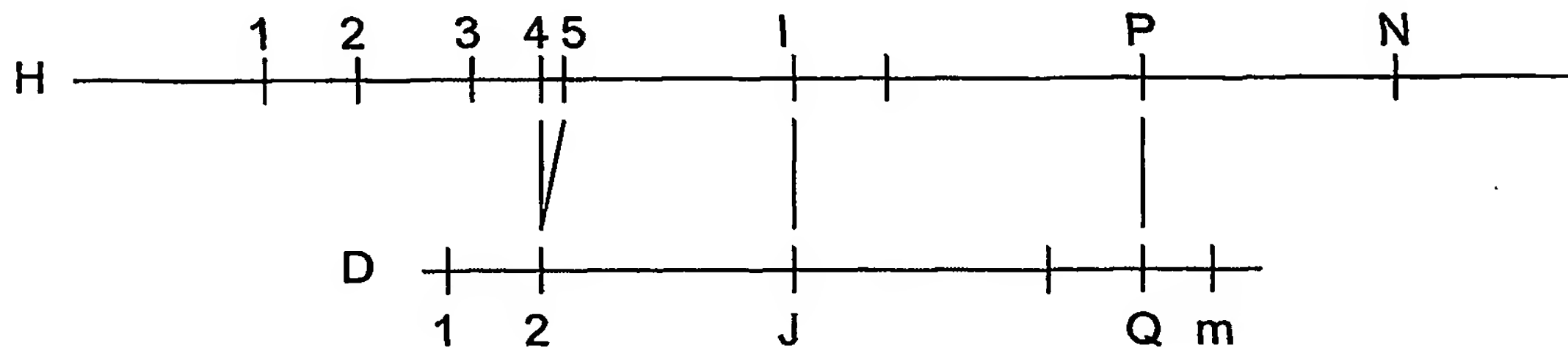
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(57) Abstract: System, process and software arrangement produces high resolution, high accuracy, ordered, genome wide haplotyped maps from single molecule based approximate ordered maps and the location of genes responsible for genetic diseases are determined by performing an association study using a population of genome wide haplotyped maps. This can also be used with Optical Mapping data to assemble a genome wide haplotyped restriction map based on multiple distinguishable restriction enzymes. This invention can also be used with any other single molecule process that can produce approximate ordered physical map from randomly broken DNA pieces of a particular genome.